Amendments to the Claims

In the claims:

Claims 1-12 (Cancelled)

13. (Currently Amended) A method of detecting the presence of an analyte nucleic acid in a sample, said method comprising:

(a) providing a nucleic acid array comprising:

(i) at least one hybridization feature to which said analyte nucleic acid specifically binds under stringent hybridization conditions; and

(ii) at least one background feature, wherein said background feature is a polymeric composition that comprises background probes that do not specifically bind under stringent hybridization conditions to **complementary nucleic acids in** ~~**any target nucleic acids of**~~ said sample;

(b) contacting said nucleic acid array with said sample under stringent hybridization conditions;

(c) washing said nucleic acid array;

(d) detecting a hybridization signal from said hybridization feature and background signal from said background feature;

(e) subtracting said background signal from said hybridization signal to obtain a background corrected hybridization signal; and

(f) relating said background corrected hybridization signal to the presence of said analyte target nucleic acid in said sample to detect the presence of said analyte target nucleic acid in said sample;

wherein said method is further characterized by including a target nucleic acid labeling step prior to said detecting step (d).

14. (Cancelled)

15. (Previously Presented) The method according to Claim 13, wherein said labeling step comprises labeling any analyte target nucleic acids present in said sample with a member of a signal producing system prior to said contacting step (b).

16. (Previously Presented) The method according to Claim 13, wherein said labeling step comprises labeling any analyte target nucleic acids present on said array following step(b) with a member of a signal producing system.

17. (Cancel)

18. (Previously Presented) The method according to Claim 13, wherein said background feature provides a background signal following said contacting step that comprises: (a) a feature substrate background component; (b) a probe background component; and (c) a non-specific binding background component.

19. (Original) The method according to Claim 18, wherein said background probes of said background feature range in length from about 5 to about 100 nt.

20. (Original) The method according to Claim 18, wherein said background probes are selected from the group consisting of empirically observed inactive probes, probes forming intramolecular structures, short probes, probes comprising reverse polarity nucleotide analogs, probes comprising abasic phosphodiesters or probes comprising modified nucleotidic units.

21. (Previously presented) The method according to Claim 13, wherein said background feature provides a signal that is the same as a signal generated by a validated background feature made up of empirically observed inactive probes.

22. (Previously Presented) The method according to Claim 21, wherein said validated background feature is made up of nucleic acids having a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 05 to 18, 24 to 32 and 36 to 53.

23. (Original) The method according to Claim 13, wherein said background feature tests positive in a two-color self-self array hybridization assay.

Claims 24-27 (Cancelled)